

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 16, 2004, 00:05:31 ; Search time 192 Seconds
(without alignments)

29.967 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLSGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : uniprot_02 : *

1: uniprot_sprot : *

2: uniprot_trembl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	45	76.3	3767 1	MUA3 CAEEL
2	43	72.9	4569 2	Q7PV66
3	42	71.2	86 2	Q9K0B9
4	42	71.2	325 2	Q7QH80
5	42	71.2	678 2	Q8MSR8
6	42	71.2	826 2	Q9VJ69
7	41	69.5	636 2	Q87RD2
8	41	69.5	639 2	Q6D4L5
9	41	69.5	639 2	Q7MML9
10	41	69.5	639 2	Q8DPR5
11	41	69.5	798 1	ITBI_HUMAN
12	41	69.5	798 1	Q8WUM6
13	41	69.5	823 2	Q7Z3V1
14	40	67.8	892 2	P91085
15	39	66.1	55 2	Q9RK17
16	39	66.1	55 2	Q9N169
17	39	66.1	74 2	Q88RT9
18	39	66.1	85 2	Q9N171
19	39	66.1	88 2	Q7MJK2
20	39	66.1	138 2	Q6IKD8
21	39	66.1	205 2	Q9Y4U5
22	39	66.1	285 2	Q8OR02
23	39	66.1	336 2	Q6NTM4
24	39	66.1	336 2	A4H68935
25	39	66.1	1129 2	Q7QKX8
26	38.5	65.3	127 2	Q9TV27
27	38.5	65.3	150 1	RNS6_AOTTR
28	38.5	65.3	150 1	RNS6_CERAE
29	38.5	65.3	150 1	RNS6_GORGO
30	38.5	65.3	150 1	RNS6_HUMAN
31	38.5	65.3	150 1	RNS6_MACMU

ALIGNMENTS

RESULT 1

ID	MUA3 CAEEL	STANDARD	PRT	3767 AA.
AC	P34576; Q21340; Q9VAL3;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	26-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Transmembrane cell adhesion receptor mna-3 precursor.			
GN	Name=mna-3; ORFNames=K08B5.3/T20G5.3;			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;			
OC	Rhabditidae; Pseudocercariae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Lu Z., Vogel B., Hedgecock E.;			
RT	"mna-3 mRNA Splicing pattern revealed.";			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Berks M., Smith A., Kershaw J.;			
RT	Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Involved in cell adhesion.			
CC	-1- SIMILARITY: Contains 52 EGF-like domains.			
CC	-1- SIMILARITY: Contains 4 LDL-receptor class A domains.			
CC	-1- SIMILARITY: Contains 1 VMPA domain.			
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcement/ or send an email to license@sib.ac.uk).			
CC	EMBL; AF139060; AAD29428.1; -			
DR	EMBL; Z30974; CAAB3226.2; -			
DR	EMBL; Z30423; CAAB3226.2; JOINED.			
DR	EMBL; Z30423; CAC42345.1; JOINED.			
DR	EMBL; Z30974; CAC42345.1; JOINED.			
DR	HSSP; Q07954; ICR8.			
DR	InterPro; IPR000152; AEG_hydroxyl_S.			
DR	InterPro; IPR000152; EGF_2.			
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR006209; EGF_Like.			
DR	InterPro; IPR002172; LDL_receptor_A.			
DR	InterPro; IPR000082; SEA.			
DR	InterPro; IPR002035; VWF_A.			
DR	Pfam; PF00006; EGF; 30.			

32	38.5	65.3	150	1	RNS6_MIOA	046531 miopithecus
33	38.5	65.3	150	1	RNS6_PANTR	046525 pan troglod
34	38.5	65.3	150	1	RNS6_PAPHA	046527 papio hamad
35	38.5	65.3	150	1	RNS6_SAGOE	046530 saguinus oe
36	38.5	65.3	150	2	CAG33246	04653246 homo sapi
37	38	64.4	114	2	Q05835	005835 homo sapien
38	38	64.4	138	2	Q82256	082256 enterococcu
39	38	64.4	149	2	Q74721	Q74721 geobacter s
40	38	64.4	149	2	AAR36515	AAR36515 geobacter
41	38	64.4	157	2	Q9V9A1	Q9V9A1 drosophila
42	38	64.4	181	2	Q6NGE4	Q6NGE4 corynebacte
43	38	64.4	181	2	CAE50107	CAE50107 corynebac
44	38	64.4	220	2	Q7N037	Q7N037 chromobacte
45	38	64.4	222	2	Q7QX77	Q7QX77 giardia lam

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DR Pfam; PF00057; ldl_recept_a; 3.
DR Pfam; PF01390; SEA; 2.
DR PRINTS; PR00261; VWA; 1.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SMO0453; VMPADOMAIN.
DR SMART; SMO0179; EGF_CA; 1.
DR SMART; SMO0192; LDLa; 5.
DR SMART; SMO0200; SEA; 2.
DR SMART; SMO0327; VWA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 32.
DR PROSITE; PS00020; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00026; EGF_3; 42.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00069; LDLRA_2; 4.
DR PROSITE; PS00024; SEA; 2.
DR PROSITE; PS0034; VMPA; 1.
DR Cell adhesion; EGF-like domain; Glycoprotein; Receptor; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 3767 Transmembrane cell adhesion receptor mu-
FT 25 3767 3. Extracellular (Potential).
FT DOMAIN 25 3417 Potential.
FT TRANSMEM 3418 3438 Cytoplasmic (Potential).
FT 3439 3767 LDL-receptor class A 1.
FT DOMAIN 26 63 LDL-receptor class A 2.
FT DOMAIN 133 166 LDL-receptor class A 3.
FT DOMAIN 167 209 LDL-receptor class A 4.
FT DOMAIN 225 268 EGF-like 1.
FT DOMAIN 375 416 EGF-like 2.
FT DOMAIN 418 466 EGF-like 3.
FT DOMAIN 468 517 EGF-like 4.
FT DOMAIN 519 566 EGF-like 5.
FT DOMAIN 614 663 EGF-like 6.
FT DOMAIN 665 713 EGF-like 7.
FT DOMAIN 714 760 EGF-like 8.
FT DOMAIN 762 810 EGF-like 9.
FT DOMAIN 816 860 EGF-like 10.
FT DOMAIN 861 908 EGF-like 11.
FT DOMAIN 910 961 EGF-like 12.
FT DOMAIN 963 1012 EGF-like 13.
FT DOMAIN 1029 1070 EGF-like 14.
FT DOMAIN 1071 1118 EGF-like 15.
FT DOMAIN 1120 1168 EGF-like 16.
FT DOMAIN 1170 1219 EGF-like 17.
FT DOMAIN 1230 1406 VMPA.
FT DOMAIN 1421 1466 EGF-like 18.
FT DOMAIN 1466 1510 EGF-like 19.
FT DOMAIN 1521 1562 EGF-like 20.
FT DOMAIN 1563 1608 EGF-like 21.
FT DOMAIN 1608 1656 EGF-like 22.
FT DOMAIN 1658 1706 EGF-like 23.
FT DOMAIN 1708 1755 EGF-like 24.
FT DOMAIN 1759 1807 EGF-like 25.
FT DOMAIN 1809 1860 EGF-like 26.
FT DOMAIN 1862 1911 EGF-like 27.
FT DOMAIN 1913 1961 EGF-like 28.
FT DOMAIN 1963 2011 EGF-like 29.
FT DOMAIN 2014 2062 EGF-like 30.
FT DOMAIN 2068 2112 EGF-like 31.
FT DOMAIN 2113 2160 EGF-like 32.
FT DOMAIN 2162 2208 EGF-like 33.
FT DOMAIN 2210 2258 EGF-like 34.
FT DOMAIN 2260 2308 EGF-like 35.
FT DOMAIN 2310 2358 EGF-like 36.
FT DOMAIN 2360 2408 EGF-like 37.
FT DOMAIN 2409 2455 EGF-like 38.
FT DOMAIN 2456 2504 EGF-like 39.
FT DOMAIN 2513 2563 EGF-like 40.
FT DOMAIN 2565 2616 EGF-like 41.
FT DOMAIN 2618 2666 EGF-like 42.
FT DOMAIN 2668 2714 EGF-like 43.
FT DOMAIN 2716 2763 EGF-like 44.
FT DOMAIN 2763 2811 EGF-like 45.
FT DOMAIN 2811 2833 EGF-like 46.
FT DOMAIN 2833 2872 EGF-like 47.
FT DOMAIN 2872 2997 SEA 1.
FT DOMAIN 2997 3048 EGF-like 48.
FT DOMAIN 3048 3172 SEA 2.
FT DOMAIN 3172 3224 EGF-like 49.
FT DOMAIN 3224 3272 EGF-like 50.
FT DOMAIN 3272 3324 EGF-like 51.
FT DOMAIN 3324 3373 EGF-like 52.
FT DOMAIN 3373 3409 calcium-binding (Potential).
FT DOMAIN 3409 243 By similarity.
FT DISULFID 229 252 By similarity.
FT DISULFID 235 287 By similarity.
FT DISULFID 254 287 By similarity.
FT DISULFID 361 382 By similarity.
FT DISULFID 386 402 By similarity.
FT DISULFID 404 415 By similarity.
FT DISULFID 422 435 By similarity.
FT DISULFID 429 444 By similarity.
FT DISULFID 446 465 By similarity.
FT DISULFID 472 486 By similarity.
FT DISULFID 480 495 By similarity.
FT DISULFID 497 516 By similarity.
FT DISULFID 523 536 By similarity.
FT DISULFID 530 545 By similarity.
FT DISULFID 547 565 By similarity.
FT DISULFID 618 632 By similarity.
FT DISULFID 626 642 By similarity.
FT DISULFID 644 662 By similarity.
FT DISULFID 669 682 By similarity.
FT DISULFID 676 691 By similarity.
FT DISULFID 693 712 By similarity.
FT DISULFID 718 729 By similarity.
FT DISULFID 723 738 By similarity.
FT DISULFID 740 759 By similarity.
FT DISULFID 766 779 By similarity.
FT DISULFID 773 788 By similarity.
FT DISULFID 790 809 By similarity.
FT DISULFID 820 836 By similarity.
FT DISULFID 848 859 By similarity.
FT DISULFID 867 879 By similarity.
FT DISULFID 885 898 By similarity.
FT DISULFID 890 907 By similarity.
FT DISULFID 914 930 By similarity.
FT DISULFID 924 939 By similarity.
FT DISULFID 941 960 By similarity.
FT DISULFID 967 981 By similarity.
FT DISULFID 975 990 By similarity.
FT DISULFID 992 1011 By similarity.
FT DISULFID 1033 1046 By similarity.
FT DISULFID 1040 1055 By similarity.
FT DISULFID 1057 1069 By similarity.
FT DISULFID 1075 1087 By similarity.
FT DISULFID 1081 1096 By similarity.
FT DISULFID 1098 1117 By similarity.
FT DISULFID 1124 1137 By similarity.
FT DISULFID 1131 1146 By similarity.
FT DISULFID 1148 1167 By similarity.
FT DISULFID 1174 1188 By similarity.
FT DISULFID 1182 1197 By similarity.
FT DISULFID 1199 1218 By similarity.
FT DISULFID 1425 1441 By similarity.
FT DISULFID 1453 1450 By similarity.
FT DISULFID 1452 1465 By similarity.
FT DISULFID 1470 1484 By similarity.
FT DISULFID 1478 1494 By similarity.
FT DISULFID 1496 1509 By similarity.
FT DISULFID 1525 1538 By similarity.
FT DISULFID 1532 1547 By similarity.
FT DISULFID 1549 1561 By similarity.
FT DISULFID 1567 1583 By similarity.
FT DISULFID 1575 1592 By similarity.
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FT DISULFID 1594 1607 By similarity.
FT DISULFID 1612 1625 By similarity.
Query Match
Best Local Similarity 76.3%; Score 45; DB 1; Length 3767;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPOC 10
DB 2088 CRLMGEPOC 2097

RESULT 2
Q7PV66 PRELIMINARY; PRT; 4569 AA.
ID Q7PV66 AC
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE ENSANGP0000011153 (Fragment).
GN Name=ENSANGG00000008664;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008986; EAA00393.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR01881; EGF_Ca.
DR InterPro; IPR06209; EGF_like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000033; LDL_receptor_rep.
DR Pfam; PF00008; EGF_12.
DR Pfam; PF07645; EGF_CA_2.
DR Pfam; PF00057; Ldl_recept_a; 28.
DR Pfam; PF00058; Ldl_recept_b; 24.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS01209; LDLRA_1; 22.
DR PROSITE; PS00068; LDLRA_2; 27.
DR EGF-like domain.
KM
FT NON_TER 1
SQ SEQUENCE 4569 AA; 509734 MW; DDC5E46D7A338522 CRC64;

Query Match
Best Local Similarity 72.9%; Score 43; DB 2; Length 4569;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPOC 10
DB 4112 CELVNGEPOC 4121

RESULT 3
Q9K0E9 PRELIMINARY; PRT; 86 AA.
ID Q9K0E9 AC
Q9K0E9;

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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein NMB0658.
GN OrderedLocustNames=NMB0658;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair B.M.,
RA Clifton H., Clark E.B., Cotton M.D., Ueberback T.R., Knout H.M.,
RA Qin H., Vamathevan J.V., Gill J., Scarlato V., Maignani V., Pizzi M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL; AE002420; AAF62315.1; -.
DR TIGR; NMB0658; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 86 AA; 9933 MW; 6CEB3DF0A5F8D0E5 CRC64;

Query Match
Best Local Similarity 71.2%; Score 42; DB 2; Length 86;
Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 CRLR--SGEPOC 10
DB 24 CRLRMSTGPOC 35

RESULT 4
Q7Q880 PRELIMINARY; PRT; 325 AA.
ID Q7Q880 AC
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP7010.
GN Name=agCG45493; ORFNames=ENSANGG00000019789;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008816; EAA05064.1; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR004094; Prot_inh_antisen.
DR InterPro; IPR001007; VWFC_C.
DR Pfam; PF02822; Antisense; 1.
DR PROSITE; PS01208; VWFC_1; UNKNOWN_1.
DR PROSITE; PS0184; VWFC_2; 1.
SQ SEQUENCE 325 AA; 35670 MW; F791C278F0C816C6 CRC64;

Query Match
Best Local Similarity 71.2%; Score 42; DB 2; Length 325;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CRISGEPC 10
DB 127 CRCEAGEPC 136

RESULT 5

ID Q8MSR8 PRELIMINARY: PRT: 678 AA.

DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE SD0507D.

GN Name=CG15165; ORFNames=CG31790;

OS Drosophila melanogaster (Fruit fly)

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OC NCBI_TaxID=7227;

RN [1]

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Stagleton M., Brckstein P., Hong L., Agbayan A., Carlson J.,

RA Foster C., Gabriellan A.E., Gary N.S., Gelbart W.M., Glaeser K.,

RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegun C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.W., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacled J.M.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stagleton M., Strong R., Sun E.,

RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.T., Wassenaar D.A., Weinstein G.M., Weisbach J.,

RA Williams S.M., Woodgett W., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodson A.,

RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Pacled J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svitskas R., Tabor P.E., Wan K., Stagleton M., Sutton G.G., Venter C.,

RA Weisskaf R., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

RT melanogaster euchromatic genome sequence."

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svitskas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.,

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomic perspective."

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [6]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

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RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [7]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [8]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [9]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [10]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [11]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [12]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [13]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [14]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,

RA Smith C.D., Tudy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stagleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

QY 1 CRLRSGEP 9
 DB 367 CRLRSGEP 375

RESULT 7
 Q87RD2 PRELIMINARY; PRT; 636 AA.
 AC Q87RD2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE ATP-dependent helicase, Ding family.
 GN OrderedLocustNames=VP0865;
 OS *Vibrio parahaemolyticus*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OC NCBI_TaxID=670;
 RX MEDLINE=22508454; PubMed=12620739;
 RX STRAIN=RIMD 2210633 / Serotype O3:k6;
 RA Wakino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Naito M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shingawa H., Hatford M., Iida T.;
 RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
 RT distinct from that of *V. cholerae*.";
 RL Lancet 361:743-749(2003).
 DR EMBL:AP005075; BAC59128.1; -;
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR GO: GO:0016818; F:hydrolyase activity, acting on acid anhydrid. .; IEA.
 DR GO: GO:0003676; P:nucleic acid binding; IEA.
 DR GO: GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. .; IEA.
 DR InterPro: IPR001410; DEAP.
 DR InterPro: IPR006555; Helic_C2.
 DR InterPro: IPR01060; RibP_Bind_barrel.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00491; HELIC_C2; 1.
 KM Complete proteome; Helicase.
 SQ SEQUENCE 636 AA; 70979 MW; B0340E15D486F1 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 636;
 Best Local Similarity 87.5%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRLRSGEP 8
 DB 560 CRLRSGEP 567

RESULT 8
 Q6D4L5 PRELIMINARY; PRT; 639 AA.
 ID Q6D4L5;
 AC Q6D4L5;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, last annotation update)
 DE Putative ATP-dependent helicase.
 GN ORFNames=EC2375;
 OS *Escherichia coli* subsp. *attenuata* SCRI1043.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OC NCBI_TaxID=218491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SCRI1043;
 RA Bell L.S., Sebailia M., Pritchard L., Holden M., Hyman L.J.,
 RA Holava M.C., Thomson N.R., Bentley S.P., Churcher C., Mungall K.,
 RA Akkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Fraser A., Hance Z., Hauser H., Jagers K., Moule S., Nordberg S.,
 RA Omond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmund G.P.C., Birch P.R.J., Barrell B.G., Parkhill J., Toth I.K.;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX50851; CAG75278.1; -;
 KW Helicase.
 SQ SEQUENCE 639 AA; 70862 MW; 727C97991C63ECB4 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 639;
 Best Local Similarity 87.5%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRLRSGEP 8
 DB 562 CRLRSGEP 569

RESULT 9
 Q7MML9 PRELIMINARY; PRT; 639 AA.
 ID Q7MML9;
 AC Q7MML9;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Rad3-related DNA helicase.
 GN Name=VVI048;
 OS *Vibrio vulnificus* (strain YJ016).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OC NCBI_TaxID=196600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=1465965;
 RA Liao C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
 RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.-B.-T., Li J.-C., Su T.-L.,
 RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
 RT "Comparative genome analysis of *Vibrio vulnificus*, a marine
 RT pathogen.";
 RL Genome Res. 13:2577-2587(2003).
 DR EMBL: AF005334; BAC93812.1; -;
 DR GO: GO:0004386; F:helicase activity; IEA.
 KM Helicase.
 SQ SEQUENCE 639 AA; 71182 MW; AE7133270150986D CRC64;

Query Match 69.5%; Score 41; DB 2; Length 639;
 Best Local Similarity 87.5%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRLRSGEP 8
 DB 560 CRLRSGEP 567

RESULT 10
 Q8DPR5 PRELIMINARY; PRT; 639 AA.
 ID Q8DPR5;
 AC Q8DPR5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Rad3-related DNA helicase.
 GN OrderedLocustNames=VVI0141;
 OS *Vibrio vulnificus*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; *Vibrio*.
 OC NCBI_TaxID=672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE016757; AAC08679.1; -;
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.

DR GO: GO:0016818; P:hydrolase activity, acting on acid anhydrid. . . ; IEA.
 DR GO: GO:0003676; P:nucleic acid binding; IEA.
 DR GO: GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. . . ; IEA.
 DR InterPro; IPR001410; DED.
 DR InterPro; IPR006555; Helic_c2.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00491; HELICC2; 1.
 KW Complete proteome; Helicase.
 SQ SEQUENCE 639 AA; 71292 MW; 9E9334E31C4E8F30 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 639;
 Best Local Similarity 87.5%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRLSGEP 8
 DB 560 CRLSGEP 567

RESULT 11
 ID ITB1_HUMAN STANDARD; PRT; 798 AA.
 AC P05556; P78466; P78467; Q13089; Q13090; Q13091; Q13212; Q14622;
 AC Q14647; P18466; P78467; Q13089; Q13090; Q13091; Q13212; Q14622;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Integrin beta-1 precursor (Fibronectin receptor beta subunit) (CD29
 DE antigen) (Integrin VIA-4 beta subunit).
 GN Name=ITGB1; Synonyms=FNRB;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA-1A).
 RC TISSUE=Placenta;
 RX MEDLINE=88007843; PubMed=2958481;
 RA Argaves W.S., Suzuki S., Arai H., Thompson K., Pieschbacher M.D.,
 RA Ruoslahti E.;
 RT "Amino acid sequence of the human fibronectin receptor.";
 RL J. Cell Biol. 105:1183-1190(1987).
 RN [2]
 RP SEQUENCE OF 717-757 FROM N.A. AND CHARACTERIZATION OF BETA-1B.
 RX MEDLINE=93209984; PubMed=7681433;
 RA Balzac F., Belkin A.M., Koteliansky V.E., Balabanov Y.V., Altruda F.,
 RA Silengo L., Tarone G.;
 RT "Expression and functional analysis of a cytoplasmic domain variant of
 the beta 1 integrin subunit.";
 RL J. Cell Biol. 121:171-178(1993).
 RN [3]
 RP SEQUENCE OF 717-757 FROM N.A. AND FUNCTION.
 RX MEDLINE=95014744; PubMed=7523423;
 RA Balzac F., Retta S.F., Albini A., Melchiorri A., Koteliansky V.E.,
 RA Genina M., Silengo L., Tarone G.;
 RT "Expression of beta 1B integrin isoform in CHO cells results in a
 dominant negative effect on cell adhesion and motility.";
 RL J. Cell Biol. 127:557-565(1994).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BETA-1A; BETA-1B; BETA-1C AND
 RP BETA-1D).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=95398646; PubMed=7545396;
 RA Zhidkova N.I., Belkin A.M., Mayne R.;
 RT "Novel isoform of beta 1 integrin expressed in skeletal and cardiac
 muscle.";
 RL Biochem. Biophys. Res. Commun. 214:279-285(1995).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1B).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=9105539; PubMed=2249781;
 RA Altruda F., Cervella P., Tarone G., Botta C., Balzac F., Stefanuto G.,
 RA Silengo L.;

RT "A human integrin beta 1 subunit with a unique cytoplasmic domain
 RT generated by alternative mRNA processing.";
 RT Gene 95:261-266(1990).
 RL [6]
 RN PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1D).
 RX MEDLINE=95377431; PubMed=7544298;
 RA van der Flier A., Kulkman I., Baudoin C., van der Neut R.,
 RA Sonnenberg A.;
 RT "A novel beta 1 integrin isoform produced by alternative splicing:
 RT unique expression in cardiac and skeletal muscle.";
 RL FEBS Lett. 369:340-344(1995).
 RN [7]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BETA-1A AND BETA-1C).
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=92202279; PubMed=1551917;
 RA Languino L.R., Ruoslahti E.;
 RT "An alternative form of the integrin beta 1 subunit with a variant
 RT cytoplasmic domain.";
 RL J. Biol. Chem. 267:7116-7120(1992).
 RN [8]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1C-2).
 RX MEDLINE=98161805; PubMed=9494094;
 RA Svingen G., Faessler R., Johansson S.;
 RT "Identification of beta1C-2, a novel variant of the integrin beta1
 RT subunit generated by utilization of an alternative splice acceptor
 RT site in exon C.";
 RL Biochem. J. 330:1255-1263(1998).
 RN [9]
 RP INTERACTION WITH LGALS3BP.
 RX PubMed=9501082;
 RA Sasaki T., Brakhus C., Engel J., Timpl R.;
 RT "Mac-2 binding protein is a cell-adhesive protein of the extracellular
 RT matrix which self-assembles into ring-like structures and binds beta1
 RT integrins, collagens and fibronectin.";
 RL EMBO J. 17:1606-1613(1998).
 RN [10]
 RP INTERACTION WITH FLNA AND FLNB, AND MUTAGENESIS OF ALA-786 AND
 RP GLY-778.
 RX PubMed=1197098; DOI=10.1093/jcb.200103037;
 RA Van der Flier A., Kulkman I., Kramer D., Geerts D., Kretz M.,
 RA Takafuta T., Shapiro S.S., Sonnenberg A.;
 RT "Different splice variants of filamin-B affect myogenesis, subcellular
 RT distribution, and determine binding to integrin (beta) subunits.";
 RL J. Cell Biol. 156:361-376(2002).
 RN [11]
 RP FUNCTION: Integrin alpha-1/beta-1, alpha-2/beta-1, alpha-5/beta-1
 and alpha-11/beta-1 are receptors for collagen. Integrins alpha-
 1/beta-1 and alpha-2/beta-1 recognize the proline-hydroxylated
 sequence G-F-P-G-E-R in collagen. Integrins alpha-2/beta-1, alpha-
 3/beta-1, alpha-4/beta-1, alpha-5/beta-1, alpha-8/beta-1, alpha-
 10/beta-1, alpha-11/beta-1 and alpha-V/beta-1 are receptors for
 fibronectin. Alpha-4/beta-1 recognizes one or more domains within
 the alternatively spliced CS-1 and CS-5 regions of fibronectin.
 Integrin alpha-5/beta-1 is a receptor for fibrinogen. Integrin
 alpha-11/beta-1, alpha-2/beta-1, alpha-6/beta-1 and alpha-7/beta-1
 are receptors for laminin. Integrin alpha-4/beta-1 is a receptor
 for VCAM1. It recognizes the sequence Q-I-D-S in VCAM1. Integrin
 alpha-9/beta-1 is a receptor for VCAM1, cytostatin and
 osteopontin. It recognizes the sequence A-E-I-D-G-I-E-L in
 cytostatin. Integrin alpha-3/beta-1 is a receptor for epiligrin
 and thrombospondin. Integrin alpha-V/beta-1 is a receptor for
 vitronectin. Beta-1 integrins recognize the sequence R-G-D in a
 wide array of ligands. Isoform beta-1B interferes with isoform
 beta-1A resulting in a dominant negative effect on cell adhesion
 and migration (in vitro).
 CC [12]
 CC SUBUNIT: Heterodimer of an alpha and a beta subunit. Beta-1
 CC associates with either alpha-1, alpha-2, alpha-3, alpha-4, alpha-
 CC 5, alpha-6, alpha-7, alpha-8, alpha-9, alpha-10, alpha-11 or
 CC alpha-V. Interacts with FLNA and FLNB. Binds LGALS3BP.
 CC [13]
 CC SUBCELLULAR LOCATION: Type I membrane protein. Isoform beta-1B
 CC does not localize to focal adhesions.
 CC [14]
 CC ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=Beta-1A;

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CC      IsoId=P05556-1; Sequence=Displayed;
CC      Name=Beta-1B;
CC      IsoId=P05556-2; Sequence=VSP_002741;
CC      Name=Beta-1C;
CC      IsoId=P05556-3; Sequence=VSP_002742;
CC      Name=Beta-1C-2;
CC      IsoId=P05556-4; Sequence=VSP_002743;
CC      Name=Beta-1D;
CC      IsoId=P05556-5; Sequence=VSP_002744;
CC      -1 TISSUE SPECIFICITY: Isoform beta-1A is widely expressed, other
CC      isoforms are generally coexpressed with a more restricted
CC      distribution. Isoform beta-1B is expressed in skin, liver,
CC      skeletal muscle, cardiac muscle, placenta, umbilical vein
CC      endothelial cells, neuroblastoma cells, lymphoma cells, hepatoma
CC      cells and astrocytoma cells. Isoforms beta-1C and beta-1C-2 are
CC      expressed in muscle, kidney, liver, placenta, cervical epithelium,
CC      umbilical vein endothelial cells, fibroblast cells, embryonal
CC      kidney cells, platelets and several blood cell lines. Isoform
CC      beta-C-2, rather than isoform beta-1C, is selectively expressed in
CC      primary T-cells. Isoform beta-1C is expressed in nonproliferating
CC      and differentiated prostate gland epithelial cells. Isoform beta-
CC      1D is expressed specifically in striated muscle (skeletal and
CC      cardiac muscle).
CC      -1 SIMILARITY: Belongs to the integrin beta chain family.
CC      -1 SIMILARITY: Contains 1 VMPA-like domain.
CC      -1 DATABASE: NAME=PROW; NOTE=CD guide CD29 entry;
CC      WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd29.htm".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC      or send an email to license@sdb-sdb.ch).
CC      -----
DR      EMBL; X07979; CAA30790.1; -
DR      EMBL; U33882; AAA79835.1; -
DR      EMBL; U33879; AAA79835.1; JOINED.
DR      EMBL; M84237; AAA74402.1; -
DR      EMBL; U33879; AAA79832.1; -
DR      EMBL; M34189; AAA59182.1; -
DR      EMBL; U33880; AAA79833.1; -
DR      EMBL; U33879; AAA79833.1; JOINED.
DR      EMBL; U28252; AAA81366.1; -
DR      EMBL; U33882; AAA79834.1; -
DR      EMBL; U33879; AAA79834.1; JOINED.
DR      EMBL; U33881; AAA79834.1; JOINED.
DR      EMBL; M84237; AAA74403.1; -
DR      PDB; 1K1L; Model; B=786-797.
DR      Genew; HGNC:6153; ITGB1.
DR      MIM; 135630; -
DR      GO; GO:0008305; C:integrin complex; NAS.
DR      GO; GO:0005515; F:protein binding; IPI.
DR      GO; GO:0046982; F:protein heterodimerization activity; NAS.
DR      GO; GO:0006968; P:cellular defense response; TAS.
DR      GO; GO:0007156; P:homophilic cell adhesion; TAS.
DR      InterPro; IPR006209; EGF-like.
DR      InterPro; IPR002369; Integrin_B.
DR      InterPro; IPR001169; Integrin_Beta_C.
DR      Pfam; PF00362; Integrin_beta_1.
DR      PRINTS; PR01166; INTEGRINB.
DR      ProDom; PD001811; Integrin_B_1.
DR      PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR      PROSITE; PS00243; INTEGRIN_BETA_3.
DR      3D-structure; Alternative splicing; Cell adhesion; Glycoprotein;
DR      Integrin; Phosphorylation; Receptor; Signal; Transmembrane.
FT      CHAIN          1          20
FT      SIGNL          1          20
FT      DOMAIN         21         728  Integrin_beta-1.
FT      TRANSMEM       729        751  Extracellular (Potential).
FT      DOMAIN         752         798  Potential.
FT      CYTOPLASMIC     799        838  Cytoplasmic (Potential).
FT      VMPA-LIKE       140         378  VMPA-like.

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FT      DOMAIN         466         635  4 cysteine-rich tandem repeats.
FT      REPEAT         466         515  1.
Query Match
Best local similarity 100.0%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      2 RLRSGEPQ 9
Db      122 RLRSGEPQ 129
RESULT 12
Q8WUM6 Q8WUM6 PRELIMINARY; PRT; 798 AA.
AC      Q8WUM6;
DT      01-MAR-2002 (TREMBLrel. 20, Created)
DT      01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Integrin beta 1, isoform 1A.
GN      Name=ITGB1;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Skin;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA      Ditchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein W.J., Udén T.B., Yoshiyuki S., Carninci P., Prange C.,
RA      Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Snevchenko Y., Bouffard G.G.,
RA      Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalski U., Smallus D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Skin;
RA      Strausberg R.;
RA      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC      -1 SIMILARITY: Belongs to the integrin beta chain family.
CC      -1 SIMILARITY: Belongs to the integrin beta chain family.
DR      EMBL; BC020057; AAH20057.1; -
DR      HSSP; P05106; IM80.
DR      GO; GO:0008305; C:integrin complex; IEA.
DR      GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR      GO; GO:0007275; P:development; IEA.
DR      GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR      InterPro; IPR006209; EGF-like.
DR      InterPro; IPR002369; Integrin_B.
DR      InterPro; IPR001169; Integrin_Beta_C.
DR      InterPro; IPR002369; Integrin_Beta_C.
DR      InterPro; IPR002035; VWF_A.
DR      Pfam; PF00362; Integrin_beta_1.
DR      PRINTS; PR01166; INTEGRINB.
DR      SMART; SM00187; INB; 1.
DR      SMART; SM00423; PSI; 1.
DR      SMART; SM00327; VWA; 1.
DR      PROSITE; PS00022; EGF_1; UNKNOWN_2.

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DR PROSITE: PS00243; INTEGRIN BETA; 3.
 KW Cell adhesion; Integrin; Transmembrane.
 SQ SEQUENCE 798 AA; 88415 MW; D835979C1625578C CRC64;

Query Match 69.5%; Score 41; DB 2; Length 798;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPC 9
 DB 122 RLRSGEPC 129

RESULT 13
 ID 0723V1 PRELIMINARY; PRT; 823 AA.

AC Q723V1.1
 DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Hypothetical protein DKFZp686D0452 (Fragment).
 GN Name=DKFZp686D0452;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC Tissue:Human endometrium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Meves H.W., Weill B., Anid C., Osanger A., Robo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to the integrin beta chain family.

DR EMBL: BX537407; CAD97649.1; -
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0008305; C:protein complex; IEA.
 DR GO: GO:0005515; F:protein binding; IEA.
 DR GO: GO:0007160; F:cell-matrix adhesion; IEA.
 DR GO: GO:0007275; P:development; IEA.
 DR GO: GO:0007229; P:integrin-mediated signaling pathway; IEA.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR002369; Integrin B.
 DR InterPro: IPR001169; Integrin_beta_C.
 DR InterPro: IPR003659; Plexin-like.
 DR InterPro: IPR02035; VWF_A.
 DR Pfam: PF00362; Integrin_beta; 1.
 DR SMART: SM00187; INB; 1.
 DR SMART: SM00423; PSI; 1.
 DR SMART: SM00327; VWA; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN 2.
 DR PROSITE: PS00243; INTEGRIN_BETA; 3.
 KW Cell adhesion; Hypothetical protein; Integrin; Transmembrane.

FT NON_TER 1
 SQ SEQUENCE 823 AA; 91130 MW; 8377A7D7C082B049 CRC64;

Query Match 69.5%; Score 41; DB 2; Length 823;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPC 9
 DB 147 RLRSGEPC 154

RESULT 14
 ID P91085 PRELIMINARY; PRT; 892 AA.
 AC P91085;
 DT 01-MAY-1997 (TRENBLREL. 03, Created)
 DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
 DE Hypothetical protein F55A12.1.

GN ORFNames=F55A12.1;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;

QY 1 CRLRSGEPC 10
 DB 511 CRLRSGEPC 520

Query Match 67.8%; Score 40; DB 2; Length 892;
 Best Local Similarity 60.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPC 10
 DB 511 CRLRSGEPC 520

RESULT 15
 ID Q9RK17 PRELIMINARY; PRT; 55 AA.
 AC Q9RK17;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
 DE Putative small membrane protein.
 GN Ordered locus names=SC03445; ORFNames=SC46.02c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteriales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieiser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL93916; CAB61853.1; -.
KW Complete proteome.
SQ SEQUENCE 55 AA; 5927 MW; BF69F887A528D263 CRC64;

Query Match 66.1%; Score 39; DB 2; Length 55;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPOC 10
| | | | |
Db 4 CLARSGEPOC 13

Search completed: December 16, 2004, 00:20:22
Job time : 194 secs

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Query Match 69.5%; Score 41; DB 2; Length 798;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSRGPQC 9
 |||||
 DB 122 RLRSRGPQC 129

RESULT 3

T15195
 Hypochemical protein F55A12.1 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T15195
 R/Pauley, A.; Galtung, S.
 Submitted to the EMBL Data Library, May 1997
 A/Description: The sequence of C. elegans cosmid F55A12.
 A/Reference number: Z18305
 A/Accession: T15195
 A/Status: preliminary; translated from GE/EMBL/DBD

A/Molecule type: DNA
 A/Residues: 1-892 <PAU>
 A/Cross-references: UNIPROT:P91085; EMBL:AF003130; NID:G2088663; PID:G2088671; PIDN:AAH5
 A/Experimental source: Strain Bristol N2; clone F55A12
 C/Keywords: CESP:F55A12.1
 A/Map position: 1
 A/Introns: 55/3; 75/3; 216/2; 460/3; 517/3; 558/1; 673/3; 753/3; 856/2

Query Match 67.8%; Score 40; DB 2; Length 892;
 Best Local Similarity 60.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSRGPQC 10
 |||||
 DB 511 CRLRSRGPQC 520

RESULT 4

S72361
 Pancreatic ribonuclease (EC 3.1.27.5) K6 precursor - human
 N/Alternate names: RNase K6
 C/Species: Homo sapiens (man)
 C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 08-May-1998
 C/Accession: S72361; S72362
 R/Rosenberg, H.F.; Dyer, K.D.
 Submitted to the EMBL Data Library, July 1996
 A/Description: Molecular cloning and characterization of a novel human ribonuclease (RNase K6)
 A/Reference number: S72361
 A/Accession: S72361
 A/Molecule type: DNA
 A/Residues: 1-150 <ROS>
 A/Cross-references: EMBL:U64998; NID:G1513101; PID:G1513102
 R/Rosenberg, H.F.; Dyer, K.D.
 Nucleic Acids Res. 24, 3507-3513, 1996

A/Title: Molecular cloning and characterization of a novel human ribonuclease (RNase K6)
 A/Reference number: S72362; MUID:56433147; PMID:8836175
 A/Accession: S72362
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 24-150 <ROW>
 A/Cross-references: EMBL:U64998
 C/Genetics:

A/Map position: 14
 A/Superfamily: pancreatic ribonuclease
 C/Keywords: glycoprotein; hydrolase; nucleic acid degradation
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-150/Product: pancreatic ribonuclease #status predicted <MAT>
 F:45-104, 60-114, 78-129, 85-97/Disulfide bonds: #status predicted
 F:55,100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.3%; Score 38.5; DB 2; Length 150;

Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSRGPQC 10
 |||||
 DB 104 CRLRSRGPQC 114

RESULT 5

JS0600
 t-Plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat
 N/Alternate names: tissue plasminogen activator
 C/Species: Desmodus rotundus (common vampire bat)
 C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C/Accession: JS0600
 R/Kraetzschmar, J.; Heindler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dor
 Gene 105, 229-237, 1991
 A/Title: The plasminogen activator family from the salivary gland of the vampire bat Des
 A/Reference number: JS0597; MUID:92039036; PMID:1937019
 A/Accession: JS0600
 A/Molecule type: mRNA
 A/Residues: 1-394 <KRA>

A/Cross-references: UNIPROT:P49150; GB:M63990; NID:G166078; PIDN:AAA31595.1; PID:G166078
 A/Note: the authors translated the codon ATC for residue 75 as Thr
 C/Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-36/Domain: propeptide #status predicted <PRO>
 F:37-394/Product: plasminogen activator gamma #status predicted <PLA>
 F:45-126/Domain: kringle homology <KR>
 F:143-388/Domain: trypsin homology <TRY>
 F:145-126, 66-108, 97-121, 131-262, 174-190, 182-251, 276-351, 308-324, 341-369/Disulfide bonds:

F:142-143/Cleavage site: His-Ser (plasmin) #status predicted
 F:189, 238, 335/Active site: His, Asp, Ser #status predicted
 F:315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.4%; Score 38; DB 2; Length 394;
 Best Local Similarity 66.7%; Pred. No. 33;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSRGPQC 10
 |||||
 DB 243 QRLRSRGPQC 251

RESULT 6

JS0599
 t-Plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat
 N/Alternate names: tissue plasminogen activator
 C/Species: Desmodus rotundus (common vampire bat)
 C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C/Accession: JS0599
 R/Kraetzschmar, J.; Heindler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dor
 Gene 105, 229-237, 1991
 A/Title: The plasminogen activator family from the salivary gland of the vampire bat Des
 A/Reference number: JS0597; MUID:92039036; PMID:1937019
 A/Accession: JS0599
 A/Molecule type: mRNA
 A/Residues: 1-431 <KRA>

A/Cross-references: UNIPROT:P49121; GB:M63989; NID:G166076; PIDN:AAA31594.1; PID:G166077
 C/Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-36/Domain: propeptide #status predicted <PRO>
 F:37-431/Product: plasminogen activator beta #status predicted <PLA>
 F:41-74/Domain: EGF homology <EGF>
 F:82-163/Domain: kringle homology <KR>
 F:180-425/Domain: trypsin homology <TRY>

F:41-52, 46-63, 65-74, 82-163, 103-145, 134-158, 168-299, 211-227, 219-288, 313-388/Disulfide bonds
 F:139, 352/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:126-180/Cleavage site: His-Ser (plasmin) #status predicted
 F:226, 275, 382/Active site: His, Asp, Ser #status predicted
 F:345-361, 378-406/Disulfide bonds: #status predicted

Query Match 64.4%; Score 38; DB 2; Length 431;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPOC 10
 DB 280 QLRSGSPQC 288

RESULT 7

t-plasminogen activator (BC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
 C:Species: Megaderma lyra
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A34369
 R:Gardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Jacob
 U: Biol. Chem. 264, 17947-17952, 1989
 A:Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasmin
 A:Reference number: A34369; NUID:90036857; PMID:2509450
 A:Accession: A34369
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-477 <GAR>
 A:Cross-references: UNIPROT:P15638; GB:J05082; NID:G166080; PIDN:AAA11596.1; PID:G166081
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-36/Domain: propeptide #status predicted <PRO>
 F:37-477/Product: plasminogen activator #status predicted <PLA>
 F:42-79/Domain: fibronectin type I repeat homology <FA>
 F:87-120/Domain: EGF homology <EGF>
 F:128-209/Domain: kringle homology <KRG>
 F:226-471/Domain: trypsin homology <TRY>
 F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
 F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 64.4%; Score 38; DB 1; Length 477;
 Best Local Similarity 66.7%; Pred. No. 40;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPOC 10
 DB 326 QLRSGSPQC 334

RESULT 8

t-plasminogen activator (BC 3.4.21.68) alpha-2 precursor - common vampire bat
 N:Alternate names: tissue plasminogen activator
 C:Species: Desmodus rotundus (common vampire bat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C:Accession: J05098
 R:Kraetzschmar, U.; Haendler, B.; Langer, G.; Boicoll, W.; Bringmann, P.; Alagon, A.; Dor
 Gene 105, 229-237, 1991
 A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des
 A:Reference number: J05097; NUID:92039036; PMID:1937019
 A:Accession: J05098
 A:Molecule type: mRNA
 A:Residues: 1-477 <KRA>
 A:Cross-references: UNIPROT:P15638; GB:M63988; NID:G166074; PIDN:AAA11593.1; PID:G166075
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-36/Domain: propeptide #status predicted <PRO>
 F:37-477/Product: plasminogen activator alpha-2 #status predicted <PLA>
 F:42-79/Domain: fibronectin type I repeat homology <FA>
 F:87-120/Domain: EGF homology <EGF>
 F:128-209/Domain: kringle homology <KRG>
 F:226-471/Domain: trypsin homology <TRY>
 F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
 F:185,398/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:225-226/Cleavage site: His-Ser (plasmin) #status predicted

F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 64.4%; Score 38; DB 2; Length 477;
 Best Local Similarity 66.7%; Pred. No. 40;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPOC 10
 DB 326 QLRSGSPQC 334

RESULT 9

PML-1 protein - human
 N:Alternate names: promyelocytic leukemia protein
 C:Species: Homo sapiens (man)
 C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
 C:Accession: A40044
 R:Kakizuka, A.; Miller Jr., W.H.; Umesono, K.; Warrell Jr., R.P.; Frankel, S.R.; Murty,
 Cell 66, 663-674, 1991
 A:Title: Chromosomal translocation t(15;17) in human acute promyelocytic leukemia fuses
 A:Reference number: A40044; NUID:91347368; PMID:1652368
 A:Accession: A40044
 A:Molecule type: mRNA
 A:Residues: 1-560 <KRA>
 A:Cross-references: UNIPROT:P29590; GB:M73778; NID:G190114; PIDN:AAA60125.1; PID:G190115
 C:Genetic: CB
 A:Gene: GDB:PML; MYL
 A:Cross-references: GDB:127542; OMIM:102578
 A:Map position: 15q22-15q22
 C:Superfamily: human PML-1 protein; RING finger homology
 C:Keywords: DNA binding; transcription regulation; zinc
 F:53-97/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 560;
 Best Local Similarity 77.8%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRGEPO 9
 DB 357 CRLRGEPO 365

RESULT 10

PML protein, splice form 2 - human
 N:Alternate names: promyelocytic leukemia protein
 C:Species: Homo sapiens (man)
 C:Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 02-Aug-2002
 C:Accession: S42517
 R:Goddard, A.D.; Borrow, J.; Freemont, P.S.; Solomon, E.
 Science 254, 1371-1374, 1991
 A:Title: Characterization of a zinc finger gene disrupted by the t(15;17) in acute prom
 A:Reference number: S42516; NUID:9207906; PMID:1720570
 A:Accession: S42517
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-589 <GDD>
 A:Cross-references: EMBL:M79463
 C:Genetic: CB
 A:Gene: GDB:PML; MYL
 A:Cross-references: GDB:127542; OMIM:102578
 A:Map position: 15q22-15q22
 C:Superfamily: human PML-1 protein; RING finger homology
 C:Keywords: zinc
 F:31-75/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 589;
 Best Local Similarity 77.8%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRGEPO 9
 DB 357 CRLRGEPO 365

Db 335 CRLRGEPO 343

RESULT 11

PM1 protein, splice form 2 - human

N/Alternate names: promyelocytic leukemia protein

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 02-Aug-2002

C/Accession: S44381

R/Godard, A.D.; Borow, J.; Freemont, P.S.; Solomon, E.

A/Description: Characterization of a novel zinc finger gene disrupted by the t(15; 17)

A/Reference number: S44380

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-589 <GOD>

A/Cross-references: EMBL:M79463; NID:g190118; PIDN:AAA60351.1; PID:g190119

C/Genetics:

A/Gene: GDB:PM1; MTL

A/Cross-references: GDB:127542; OMIM:102578

A/Map position: 15q22-15q22

C/Superfamily: human PM1-1 protein; RING finger homology

C/Keywords: zinc

F:31-75/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 589;

Best Local Similarity 77.8%; Pred. No. 48;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CRLRGEPO 9

335 CRLRGEPO 343

RESULT 12

MY1 protein - human

C/Species: Homo sapiens (man)

C/Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 09-Jul-2004

C/Accession: A60198

R/Pandolfi, P.P.; Grignani, F.; Alcalay, M.; Mencarelli, A.; Biondi, A.; Lococo, F.; Grignani, F.

A/Title: Structure and origin of the acute promyelocytic leukemia myl/RARalpha cDNA and

A/Reference number: A60198; MUID:91319412; PMID:1650447

A/Accession: A60198

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-589 <PAN>

A/Cross-references: UNIPROT:Q9BZY3

A/Note: the authors' translation is shown for residues 543-549; the corresponding nucle

C/Keywords: zinc

F:31-75/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 589;

Best Local Similarity 77.8%; Pred. No. 48;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CRLRGEPO 9

335 CRLRGEPO 343

RESULT 13

probable transcription factor PM1 S - human

C/Species: Homo sapiens (man)

C/Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004

C/Accession: B40045

R/de The, H.; Lavanu, C.; Marchio, A.; Chomienne, C.; Degos, L.; Dejean, A.

Cell 66, 675-684, 1991

A/Title: The PM1-RARalpha fusion mRNA generated by the t(15;17) translocation in acute

A/Reference number: A40045; MUID:91347369; PMID:1652369

A/Accession: B40045

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-593 <DE2>

A/Cross-references: UNIPROT:Q8WU40

C/Superfamily: human PM1-1 protein; RING finger homology

C/Keywords: zinc

F:53-97/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 593;

Best Local Similarity 77.8%; Pred. No. 48;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CRLRGEPO 9

357 CRLRGEPO 365

RESULT 14

Gene MY1 protein - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C/Accession: S19244

R/Kastner, P.; Perez, A.; Lutz, Y.; Rochette-Egly, C.; Gaub, M.P.; Durand, B.; Lanotte, E.

A/Title: Structure, localization and transcriptional properties of two classes of retino

A/Reference number: S19244; MUID:92164652; PMID:1311253

A/Accession: S19244

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-633 <KAS>

A/Cross-references: UNIPROT:P29590; EMBL:X63131; NID:G34813; PIDN:CAA44841.1; PID:G34814

C/Superfamily: human PM1-1 protein; RING finger homology

C/Keywords: DNA binding; transcription regulation; zinc

F:53-97/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 633;

Best Local Similarity 77.8%; Pred. No. 51;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CRLRGEPO 9

357 CRLRGEPO 365

RESULT 15

probable DEAD box family helicase YPO2071 [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C/Accession: AG0252

R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AG0252

A/Accession: AG0252

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-634 <KUR>

A/Cross-references: UNIPROT:Q8ZET2; GB:AL590842; PIDN:CAC90883.1; PID:g15980082; GSPDB:C

C/Genetics:

A/Gene: YPO2071

Query Match 64.4%; Score 38; DB 2; Length 634;

Best Local Similarity 75.0%; Pred. No. 52;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Thu Dec 16 12:15:14 2004

us-09-615-624a-1.rpr

Page 5

Qy 1 CRISCEP 8
| | | | |
Db 557 CRISCEP 564

Search completed: December 16, 2004, 00:17:03
Job time : 39 secs

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Thu Dec 16 12:15:13 2004

us-09-615-624a-1.rapb

Page 1

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 16, 2004, 00:13:56 ; Search time 144 Seconds
(without alignments)
24,804 Million cell updates/sec

Title: US-09-615-624A-1

Perfect score: 59

Sequence: 1 CRLRGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	76.3	3051	14 US-10-369-493-5866	Sequence 5866, App
2	41	69.5	226	16 US-10-716-293-99	Sequence 99, Appl
3	41	69.5	533	9 US-09-778-927A-67	Sequence 67, Appl
4	41	69.5	662	9 US-09-778-927A-66	Sequence 66, Appl
5	41	69.5	798	13 US-10-100-912-6	Sequence 6, Appl
6	41	69.5	798	13 US-10-072-841-30	Sequence 30, Appl
7	41	69.5	798	14 US-10-219-631-30	Sequence 30, Appl
8	41	69.5	798	14 US-10-295-027-6	Sequence 6, Appl
9	41	69.5	798	14 US-10-295-027-728	Sequence 728, App
10	41	69.5	798	15 US-10-211-462-8	Sequence 8, Appl
11	41	69.5	798	16 US-10-706-265-4	Sequence 4, Appl
12	41	69.5	819	16 US-10-408-765A-2997	Sequence 2997, Ap
13	41	69.5	835	15 US-10-425-114-39333	Sequence 39333, A

14	38	64.4	84	17 US-10-425-115-333757	Sequence 333757,
15	38	64.4	99	17 US-10-425-115-2282813	Sequence 2282813,
16	38	64.4	146	17 US-10-425-115-229690	Sequence 229690,
17	38	64.4	350	15 US-10-425-114-56245	Sequence 56245, A
18	38	64.4	354	17 US-10-425-115-337354	Sequence 337354,
19	38	64.4	759	15 US-10-755-889-384	Sequence 384, App
20	38	64.4	847	15 US-10-425-114-39243	Sequence 39243, A
21	37	62.7	36	14 US-10-072-602B-562	Sequence 247, App
22	37	62.7	36	14 US-10-072-602B-562	Sequence 562, App
23	37	62.7	50	17 US-10-425-115-251706	Sequence 251706,
24	37	62.7	62	17 US-10-425-115-34727	Sequence 314727,
25	37	62.7	82	14 US-10-072-602B-246	Sequence 246, App
26	37	62.7	106	17 US-10-425-115-369307	Sequence 369307,
27	37	62.7	112	17 US-10-425-115-190858	Sequence 190858,
28	37	62.7	147	17 US-10-425-115-274190	Sequence 274190,
29	37	62.7	159	15 US-10-424-599-145757	Sequence 145757,
30	37	62.7	263	9 US-09-141-027-2	Sequence 2, Appl
31	37	62.7	263	13 US-10-101-392-2	Sequence 2, Appl
32	37	62.7	263	13 US-10-066-500-41	Sequence 41, Appl
33	37	62.7	263	13 US-10-053-107-4	Sequence 4, Appl
34	37	62.7	263	14 US-10-028-072-484	Sequence 484, App
35	37	62.7	263	14 US-10-140-808-484	Sequence 484, App
36	37	62.7	263	14 US-10-121-042-484	Sequence 484, App
37	37	62.7	263	14 US-10-123-904-484	Sequence 484, App
38	37	62.7	263	14 US-10-140-470-484	Sequence 484, App
39	37	62.7	263	14 US-10-175-746-484	Sequence 484, App
40	37	62.7	263	14 US-10-176-918-484	Sequence 484, App
41	37	62.7	263	14 US-10-176-921-484	Sequence 484, App
42	37	62.7	263	14 US-10-002-796-41	Sequence 41, Appl
43	37	62.7	263	14 US-10-066-273-41	Sequence 41, Appl
44	37	62.7	263	14 US-10-066-494-41	Sequence 41, Appl
45	37	62.7	263	14 US-10-137-865-484	Sequence 484, App

ALIGNMENTS

RESULT 1
US-10-369-493-5866
; Sequence 5866, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10152052/B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5866
; LENGTH: 3051
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5866

Query Match 76.3% Score 45; DB 14; Length 3051;
Best Local Similarity 70.0% Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRGEPQC 10
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DB 1372 CRLMGEPKC 1381

RESULT 2
US-10-716-293-99
; Sequence 99, Application US/10716293

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; Publication No. US20040127416A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents, acting for and on behalf of,
; APPLICANT: Arizona State University (ASU)
; APPLICANT: Maesla, Stephen P.
; APPLICANT: Ehteshami, Gholam R.
; TITLE OF INVENTION: Bioselective bioconjugates for
; FILE REFERENCE: 110588.00025
; CURRENT APPLICATION NUMBER: US/10/716,293
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/295,734
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Integrin
US-10-716-293-99

Query Match          69.5%; Score 41; DB 16; Length 236;
Best Local Similarity 100.0%; Pred. No. 81;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLRSGEPQ 9
Db      122 RLRSGEPQ 129

RESULT 3
US-09-778-927A-67
; Sequence 67, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL134541
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(543)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-67

Query Match          69.5%; Score 41; DB 9; Length 543;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLRSGEPQ 9
Db      122 RLRSGEPQ 129

RESULT 4
US-09-778-927A-66
; Sequence 66, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
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; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL134541
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(662)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-66

Query Match          69.5%; Score 41; DB 9; Length 662;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLRSGEPQ 9
Db      122 RLRSGEPQ 129

RESULT 5
US-10-100-912-6
; Sequence 6, Application US/10100912
; Publication No. US20020137459A1
; GENERAL INFORMATION:
; APPLICANT: Gellier, Herbert M.
; TITLE OF INVENTION: Neurite Outgrowth and Guidance by Tenascin-C
; FILE REFERENCE: 601-1-094
; CURRENT APPLICATION NUMBER: US/10/100,912
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: PCT/US00/11647
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/132,137
; PRIOR FILING DATE: 1999-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-100-912-6

Query Match          69.5%; Score 41; DB 13; Length 798;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLRSGEPQ 9
Db      122 RLRSGEPQ 129

RESULT 6
US-10-072-841-30
; Sequence 30, Application US/10072841
; Publication No. US20020164708A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pytela, Robert
; TITLE OF INVENTION: A Nc. US20020164708A1e1 Integrin Beta Subunit and Uses
; Thereof
```

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Pretty, Schroeder, Brueggemann & Clark
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/072,841
FILING DATE: 06-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,215
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 8717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-072-841-30
Query Match 69.5%; Score 41; DB 13; Length 798;
Best Local Similarity 100.0%; Pred.No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLRSGEPO 9
Db 122 RLRSGEPO 129
RESULT 7
US-10-219-631-30
Sequence 30, Application US/10219631
Publication No. US20030064471A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
Quaranta, Vito
Pyrela, Robert
TITLE OF INVENTION: A Novel Integrin Beta Subunit and Uses
Thereof
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Pretty, Schroeder, Brueggemann & Clark
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/219,631
FILING DATE: 14-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/728,215
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 8717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-219-631-30
Query Match 69.5%; Score 41; DB 14; Length 798;
Best Local Similarity 100.0%; Pred.No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLRSGEPO 9
Db 122 RLRSGEPO 129
RESULT 8
US-10-295-027-6
Sequence 6, Application US/10295027
Publication No. US2003023350A1
GENERAL INFORMATION:
APPLICANT: Afari, Daniel
Aziz, Nacasha
Ginsberg, Wendy M.
Gish, Kurt C.
Glynn, Richard
Hevizi, Peter A.
Mack, David H.
Murray, Richard
Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
File Reference: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 6
LENGTH: 798
TYPE: PRT

ORGANISM: Homo sapiens
US-10-295-027-6

Query Match 69.5%; Score 41; DB 14; Length 798;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPQ 9
DB 122 RLRSGEPQ 129

RESULT 9
US-10-295-027-728

Sequence 728, Application US/10295027
Publication No. US2003023350A1

GENERAL INFORMATION:

APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Glash, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevazi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 728
LENGTH: 798
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-728

Query Match 69.5%; Score 41; DB 14; Length 798;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPQ 9
DB 122 RLRSGEPQ 129

RESULT 10
US-10-211-462-8
Sequence 8, Application US/10211462

Publication No. US2004003495A1

GENERAL INFORMATION:

APPLICANT: Murray, Richard
APPLICANT: Glynn, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Aziz, Natasha
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
FILE REFERENCE: 018501-006200US
CURRENT APPLICATION NUMBER: US/10/211,462
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US 09/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/334,244
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 230
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 798
TYPE: PRT
ORGANISM: Homo sapiens
US-10-211-462-8

Query Match 69.5%; Score 41; DB 15; Length 798;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPQ 9
DB 122 RLRSGEPQ 129

RESULT 11
US-10-706-265-4

Sequence 4, Application US/10706265
Publication No. US20040132642A1

GENERAL INFORMATION:

APPLICANT: Huang, Sam
TITLE OF INVENTION: METHODS OF INHIBITING METASTASIS OR GROWTH OF A TUMOR CELL
FILE REFERENCE: 224738
CURRENT APPLICATION NUMBER: US/10/706,265
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/425,472
PRIOR FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/511,581
PRIOR FILING DATE: 2003-10-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 798
TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-265-4

Query Match 69.5%; Score 41; DB 16; Length 798;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPQ 9
DB 122 RLRSGEPQ 129

RESULT 12
US-10-408-765A-2997
Sequence 2997, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:

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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Marnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2997
LENGTH: 819
TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-2997
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Query Match          69.5%; Score 41; DB 16; Length 819;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 RLRSRGPQ 9
Db 122 RLRSRGPQ 129
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RESULT 13
US-10-425-114-39333
Sequence 39333, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39333
LENGTH: 835
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB3080-056-E12_FLI.pep
US-10-425-114-39333
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 RLRSRGPQ 9
Db 159 RLRSRGPQ 166
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RESULT 14
US-10-425-115-333757
Sequence 333757, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 333757
LENGTH: 84
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_67499C.1.pep
US-10-425-115-333757
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Best Local Similarity 77.8%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CRLRSRGPQ 9
Db 9 CGLRSRGPQ 17
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RESULT 15
US-10-425-115-292813
Sequence 292813, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369328
SEQ ID NO 292813
LENGTH: 99
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_30127C.1.pep
US-10-425-115-292813
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Query Match          64.4%; Score 38; DB 17; Length 99;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CRLRSRGPQ 9
Db 31 CRLRSRGPQ 39
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Job time : 146 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2004, 00:16:26 (Search time 37 Seconds

(without alignments/sec
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Title: US-09-615-624a-1

Perfect score: 59

Sequence: 1 CRLRSGEPQC 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	69.5	798	2	US-07-728-215-30
2	41	69.5	798	3	US-08-938-085A-30
3	41	69.5	798	4	US-10-072-844-30
4	41	69.5	798	4	US-10-072-838-30
5	41	69.5	798	4	US-10-072-841A-30
6	41	69.5	798	4	US-10-219-631-30
7	39	66.1	179	1	US-07-668-648-8
8	39	66.1	179	2	US-08-429-998-8
9	39	66.1	179	2	US-08-431-333-8
10	39	66.1	179	5	PCT-US91-02321-8
11	39	66.1	271	4	US-09-252-991A-23448
12	38.5	65.3	150	2	US-08-867-676-3
13	38.5	65.3	150	2	US-08-867-676-1
14	38	64.4	144	4	US-09-134-000C-6439
15	38	64.4	404	4	US-09-489-039A-12117
16	38	64.4	477	2	US-08-560-098A-51
17	38	64.4	560	5	US-08-095-728B-6
18	38	64.4	560	5	PCT-US92-02320A-6
19	38	64.4	640	4	US-09-489-038A-14146
20	38	64.4	797	5	US-08-095-728B-2
21	38	64.4	797	5	PCT-US92-02320A-2
22	38	64.4	882	4	US-09-538-092-1036
23	37	62.7	71	4	US-08-972-408-4
24	37	62.7	71	4	US-09-267-409-4
25	37	62.7	139	4	US-09-252-991A-11205
26	37	62.7	183	4	US-09-252-991A-25989
27	37	62.7	263	2	US-08-972-008-2

28	37	62.7	263	3	US-09-141-027-2	Sequence 2, Appl
29	37	62.7	263	4	US-09-267-409-2	Sequence 2, Appl
30	37	62.7	263	4	US-09-617-804-2	Sequence 2, Appl
31	37	62.7	263	4	US-10-140-002-484	Sequence 484, App
32	37	62.7	390	4	US-09-252-991A-27049	Sequence 27049, A
33	36	61.0	458	4	US-09-843-905A-15	Sequence 15, Appl
34	36	61.0	472	2	US-08-272-255-10	Sequence 10, Appl
35	36	61.0	472	3	US-08-964-268-4	Sequence 4, Appl
36	36	61.0	472	4	US-09-105-254-4	Sequence 4, Appl
37	36	61.0	472	5	PCT-US95-08565-10	Sequence 10, Appl
38	36	61.0	517	4	US-09-252-991A-18129	Sequence 18129, A
39	36	61.0	880	4	US-09-252-991A-27741	Sequence 27741, A
40	35	59.3	66	4	US-09-270-767-36412	Sequence 36412, A
41	35	59.3	66	4	US-09-270-767-51629	Sequence 51629, A
42	35	59.3	94	4	US-09-489-039A-10376	Sequence 10376, A
43	35	59.3	143	4	US-09-252-991A-28318	Sequence 28318, A
44	35	59.3	184	4	US-09-270-767-47801	Sequence 47801, A
45	35	59.3	408	4	US-09-489-039A-9704	Sequence 9704, Ap

ALIGNMENTS

RESULT 1
US-07-728-215-30
Sequence 30, Application US/07728215
Patent No. 5962643
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Pytel, Robert
TITLE OF INVENTION: A No. 5962643e1 Integrin Beta Subunit and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Pretty, Schroeder, Bruggemann & Clark
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07728,215
FILING DATE: 19910711
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 8717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: AMINO ACID
STRANDNESS: single
TOPOLOGY: linear
US-07-728-215-30
Query Match 69.5%; Score 41; DB 2; Length 798;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 2 RLRSGEPQ 9
Db 122 RLRSGEPQ 129

RESULT 2
US-08-938-085A-30
Sequence 30, Application US/06938085A
Patent No. 6339148
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Pytela, Robert
TITLE OF INVENTION: A No. 6339148e1 Integrin Beta Subunit and Uses
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,085A
FILING DATE: 26-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,215
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 023070-080210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-938-085A-30
Query Match 69.5%; Score 41; DB 3; Length 798;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLRSGEPO 9
DB 122 RLRSGEPO 129
RESULT 3
US-10-072-844-30
Sequence 30, Application US/10072844
Patent No. 6576432
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Pytela, Robert
TITLE OF INVENTION: A No. 6576432e1 Integrin Beta Subunit and Uses
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/072,844
FILING DATE: 06-Feb-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/938,085A
FILING DATE: 26-SEP-1997
APPLICATION NUMBER: US 07/728,215
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 023070-080210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-072-844-30
Query Match 69.5%; Score 41; DB 4; Length 798;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLRSGEPO 9
DB 122 RLRSGEPO 129
RESULT 4
US-10-072-838-30
Sequence 30, Application US/10072838
Patent No. 6586277
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
APPLICANT: Quaranta, Vito
APPLICANT: Pytela, Robert
TITLE OF INVENTION: A No. 6586277e1 Integrin Beta Subunit and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESS: Pretty, Schroeder, Brueggemann & Clark
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/072,838
FILING DATE: 06-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,215
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 8717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-072-838-30

Query Match 69.5%; Score 41; DB 4; Length 798;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPO 9
Db 122 RLRSGEPO 129

RESULT 5
US-10-072-841A-30
Sequence 30, Application US/10072841A
Patent No. 6639056
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
Quaranta, Vito
Pyrela, Robert
TITLE OF INVENTION: A No. 6639056e1 Integrin Beta Subunit and Uses
Thereof
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/072,841A
FILING DATE: 02-Jun-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/938,085A
FILING DATE: 26-SEP-1997
APPLICATION NUMBER: US 07/728,215
FILING DATE: 11-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 023070-080210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-072-841A-30

Query Match 69.5%; Score 41; DB 4; Length 798;

Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPO 9
Db 122 RLRSGEPO 129

RESULT 6
US-10-219-631-30
Sequence 30, Application US/10219631
Patent No. 6787322
GENERAL INFORMATION:
APPLICANT: Sheppard, Dean
Quaranta, Vito
Pyrela, Robert
TITLE OF INVENTION: A No. 6787322e1 Integrin Beta Subunit and Uses
Thereof
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/219,631
FILING DATE: 14-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,215
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P31 8717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-219-631-30

Query Match 69.5%; Score 41; DB 4; Length 798;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPO 9
Db 122 RLRSGEPO 129

RESULT 7
US-07-668-648-8
Sequence 8, Application US/07668648
Patent No. 5416192
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
Gregory D.
TITLE OF INVENTION: NOVEL CYSTEINE-RICH GROWTH
MODULATING PROTEINS
NUMBER OF SEQUENCES: 12

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/668,648
;; FILING DATE: 19910819
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mistrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)790-9090
;; TELEFAX: (212) 869-9741
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 179 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-07-668-648-8
;
Query Match 66.1%; Score 39; DB 1; Length 179;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
QY 1 CRLSGEPOC 10
|||:|||||
DB 151 CRLSGEWAC 160
;
RESULT 8
US-08-429-998-8
; Sequence 8, Application US/08429998
; Patent No. 5885961
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,998
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;; US-08-431-333-8
;
Query Match 66.1%; Score 39; DB 2; Length 179;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
QY 1 CRLSGEPOC 10
|||:|||||
DB 151 CRLSGEWAC 160

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)790-9090
;; TELEFAX: (212) 869-9741
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 179 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-429-998-8
;
Query Match 66.1%; Score 39; DB 2; Length 179;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
QY 1 CRLSGEPOC 10
|||:|||||
DB 151 CRLSGEWAC 160
;
RESULT 9
US-08-431-333-8
; Sequence 8, Application US/08431333
; Patent No. 5965723
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; TITLE OF INVENTION: EPIITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,333
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;; US-08-431-333-8
;
Query Match 66.1%; Score 39; DB 2; Length 179;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
;
QY 1 CRLSGEPOC 10
|||:|||||
DB 151 CRLSGEWAC 160

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RESULT 10
PCT-US91-02321-8
; Sequence 8 Application PC/TUS9102321
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plowman, Gregory D.
; TITLE OF INVENTION: EPITHELIALS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biscuit-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02321
; FILING DATE: 19910403
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0071A-PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)728-4800
; TELEFAX: (206)448-4775
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-02321-8

Query Match          66.1%; Score 39; DB 5; Length 179;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRUSGEPOC 10
DB 151 CRUSGEPOC 160

RESULT 11
US-09-252-991A-23448
; Sequence 23448, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGNOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23448
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23448

Query Match          66.1%; Score 39; DB 4; Length 271;
Best Local Similarity 60.0%; Pred. No. 36;
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Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRUSGEPOC 10
DB 122 CRUSGEPOC 131

RESULT 12
US-08-867-676-3
; Sequence 3, Application US/08867676
; Patent No. 5866119
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW HUMAN RIBONUCLEASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,676
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0304 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 1513102
US-08-867-676-3

Query Match          65.3%; Score 38.5; DB 2; Length 150;
Best Local Similarity 72.7%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRUSGE-POC 10
DB 104 CRUSGE-POC 114

RESULT 13
US-08-867-676-1
; Sequence 1, Application US/08867676
; Patent No. 5866119
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW HUMAN RIBONUCLEASE
```

```

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,676
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0304 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 163 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SININOT01
CLONE: 2181484
US-08-867-676-1

Query Match 65.3%; Score 38.5; DB 2; Length 163;
Best Local Similarity 72.7%; Pred. No. 27;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLSGE-POC 10
Db 104 CRLTSGKYPQC 114

RESULT 14
US-09-134-000C-6439
Sequence 6439, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6439
LENGTH: 144
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6439

Query Match 64.4%; Score 38; DB 4; Length 144;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CRLSGEPQ 9
Db 94 CYLESGEPQ 102

RESULT 15
US-09-489-039A-12117
Sequence 12117, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12117
LENGTH: 404
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12117

Query Match 64.4%; Score 38; DB 4; Length 404;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPOC 10
Db 95 KARSSEPRC 103

Search completed: December 16, 2004, 00:26:20
Job time : 38 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2004, 00:13:26 ; Search time 159 Seconds
(without alignments)
22.562 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLRSGEPQC 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	10	4	AA46753 MMP-9 ant
2	45	76.3	10	4	AB46754 MMP-9 ant
3	42	71.2	2091	4	AB70224 Drosophila
4	41	69.5	236	8	ADO41511 Therapeut
5	41	69.5	236	8	ADP96089 Human bin
6	41	69.5	543	5	ABG70367 Novel hum
7	41	69.5	662	5	ABG70366 Novel hum
8	41	69.5	738	6	ABU03459 Angiogene
9	41	69.5	738	4	AB36837 Human int
10	41	69.5	798	4	AA39360 Human pol
11	41	69.5	798	6	ABR81864 Human int
12	41	69.5	798	6	ABU07462 Protein d
13	41	69.5	798	6	ABU07412 Protein d
14	41	69.5	798	7	ADA21004 Human bet
15	41	69.5	798	7	ADA46003 Human pro
16	41	69.5	798	7	AD38688 Cancer/an
17	41	69.5	798	7	AD39410 Cancer/an
18	41	69.5	798	8	ADQ14482 Human bet
19	41	69.5	805	4	AA41146 Human pol
20	41	69.5	819	7	AD71191 Human hea
21	41	69.5	819	8	ADW9595 Human int
22	41	69.5	963	2	AAW70540 Integrin
23	40	67.8	62	4	ABG29623 Novel hum
24	40	67.8	145	4	ABG21707 Novel hum
25	40	67.8	191	4	ABG21688 Novel hum

26	40	67.8	205	4	ABG21679	Abg21679 Novel hum
27	40	67.8	207	4	ABG21676	Abg21676 Novel hum
28	40	67.8	247	4	ABG21675	Abg21675 Novel hum
29	40	67.8	257	4	ABG21680	Abg21680 Novel hum
30	40	67.8	1043	4	ABG06467	Abg06467 Novel hum
31	39	66.1	110	4	AB46755	MMP-9 ant
32	39	66.1	110	4	AA39360	Human pol
33	39	66.1	128	2	AA415426	Bovine ep
34	39	66.1	228	4	AA40688	Human pol
35	39	65.3	271	7	ABO74702	Pseudomon
36	38.5	65.3	150	7	ADC78233	Human sec
37	38.5	65.3	163	6	AAW8487	Human rib
38	38	64.4	16	6	ABP9812	Human sec
39	38	64.4	16	6	ABR01302	Human gen
40	38	64.4	16	6	ADA98380	Human sec
41	38	64.4	16	7	ADC20545	Human sec
42	38	64.4	17	3	AA352042	Human sec
43	38	64.4	144	7	ADH88554	Enterococ
44	38	64.4	157	4	AB370321	Drosophila
45	38	64.4	230	4	ABG25277	Novel hum

ALIGNMENTS

RESULT 1
ID AA46753 standard; peptide; 10 AA.
XX
AC AA46753:
XX
DT 12-Apr-2001 (first entry)
XX
DE MMP-9 antagonist peptide FRIP-1.
XX
XX Antagonist; MMP-9; inhibition; angiogenesis; tumor growth; beta-integrin;
KW protein-protein interaction; matrix metalloproteinase; cytosolic; sarcoma;
KW antitumor; antiproliferative; vasodilator; antidiabetic; osteoporosis; glioma;
KW anti-rheumatoid; antiarthritic; antithrombotic; antithrombotic; ophthalmologic;
KW neuroinflammatory; metastasis; psoriasis; macular degeneration;
KW neurological disease; retinopathy; melanoma; carcinoma; fibrosarcoma;
KW astrocytoma; diabetic retinopathy; neovascular glaucoma; osteoporosis;
KW atherosclerotic plaques; rheumatoid arthritis.
XX
OS Synthetic.
XX
PN MO200104157-A2.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000MO-US019095.
XX
PR 13-JUL-1999; 99US-0143581P.
XX 02-SEP-1999; 99US-0152495P.
XX
FA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
XX Brooks PC, Haasaneh L, Rodriguez D;
XX WPL; 2001-138319/14.
XX
PT Novel antagonist inhibiting angiogenesis by modifying protein-protein
PT interactions, specifically matrix metalloproteinase-9 - beta1 containing
PT integrin interaction, useful to inhibit psoriasis, macular degeneration.
XX
PS Claim 27, Page 60; 61pp; English.
XX
CC This invention describes a novel antagonist (I) that inhibits
CC angiogenesis and/or tumor growth by modifying protein-protein
CC interactions which specifically binds to matrix metalloproteinase (MMP)-9
CC or beta-1 integrin. The products of the invention have cytostatic,
CC antitumor, antiproliferative, vasodilator, antidiabetic, osteoporotic, anti-
CC rheumatoid, antiarthritic, antithrombotic, antithrombotic, ophthalmologic and

antiinflammatory activity. (1) inhibits angiogenesis, tumor growth, metastasis, or a disease state such as psoriasis, macular degeneration, neurological disease, or restenosis in a tissue. (1) is useful for inhibiting angiogenesis, in a mammalian arthritic, ocular, retinal, or hemangioma tissue which is inflamed and angiogenesis is occurring. (1) is also useful for inhibiting tumor growth or metastasis such as melanoma, carcinoma, sarcoma, fibrosarcoma, glioma, or astrocytoma, in a tissue. (1) is also useful for inhibiting psoriasis, macular degeneration or restenosis in a tissue. In all the above conditions, (1) is administered in conjunction with chemotherapy or radiation. (1) is also useful for detecting angiogenesis and detecting tumors or tumor invasion in a tissue ex vivo. The antagonist in this case is conjugated to fluorochrome, radioactive tag, paramagnetic heavy metal, diagnostic dye or enzyme. (1) is also useful for treating diabetic retinopathy, neovascular glaucoma, atherosclerotic plaques, osteoporosis, rheumatoid arthritis and other inflammatory diseases. The method are effective in part because the therapy is highly selective for angiogenesis and no other biological processes. Only new vessel growth is inhibited by antagonists that disrupt the localization of MMP-9, and therefore the therapeutic methods do not adversely affect mature vessels. Also, because certain of (1) affect only the localization of MMP-9, and do not directly block the proteolytic activity of MMP-9 or the adhesive functions of the beta1 integrins, it is likely that these compounds will have fewer side effects because the proteolytic activity of MMP-9 or the adhesive functions of the beta1 integrins may have normal physiological functions. The antagonists are highly potent suggesting that they may have therapeutic benefits at low concentrations

Sequence 10 AA;

Query Match 100.0%; Score 59; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.006; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 CRLSGEPQC 10
1 CRLSGEPQC 10

RESULT 2
AAB46754
ID AAB46754 standard; peptide; 10 AA.

AC AAB46754;
DT 12-APR-2001 (first entry)
DE MMP-9 antagonist peptide AAA.

Antagonist; MMP-9; inhibition; angiogenesis; tumor growth; beta-integrin; protein-protein interaction; matrix metalloproteinase; cytosolic; sarcoma; anti-tumor; anti-psoriasis; vasotropic; antidiabetic; osteopathic; glioma; anti-rheumatoid; anti-arthritic; anti-atherosclerotic; ophthalmological; anti-inflammatory; metastasis; psoriasis; macular degeneration; neurological disease; restenosis; melanoma; fibrosarcoma; astrocytoma; diabetic retinopathy; neovascular glaucoma; osteoporosis; atherosclerotic plaques; rheumatoid arthritis.

Synthetic.

WO200104157-A2.

18-JAN-2001.

13-JUL-2000; 2000WO-US019095.

13-JUL-1999; 99US-0143581P.

02-SEP-1999; 99US-0152495P.

(USC-) UNIV SOUTHERN CALIFORNIA.
Brooks PC, Hassenieh L, Rodriguez D;

WPI; 2001-136319/14.
Novel antagonist inhibiting angiogenesis by modifying protein-protein interactions, specifically matrix metalloproteinase-9 - beta1 containing integrin interaction, useful to inhibit psoriasis, macular degeneration.
Example 7; Page 60; 61pp; English.

This invention describes a novel antagonist (1) that inhibits angiogenesis and/or tumor growth by modifying protein-protein interactions which specifically binds to matrix metalloproteinase (MMP)-9 or beta-1 integrin. The products of the invention have cytostatic, anti-tumor, anti-psoriasis, vasotropic, antidiabetic, osteopathic, anti-rheumatoid, anti-arthritic, anti-atherosclerotic, ophthalmological and anti-inflammatory activity. (1) inhibits angiogenesis, tumor growth, metastasis, or a disease state such as psoriasis, macular degeneration, neurological disease, or restenosis in a tissue. (1) is useful for inhibiting angiogenesis, in a mammalian arthritic, ocular, retinal, or hemangioma tissue which is inflamed and angiogenesis is occurring. (1) is also useful for inhibiting tumor growth or metastasis such as melanoma, carcinoma, sarcoma, fibrosarcoma, glioma, or astrocytoma, in a tissue. (1) is also useful for inhibiting psoriasis, macular degeneration or restenosis in a tissue. In all the above conditions, (1) is administered in conjunction with chemotherapy or radiation. (1) is also useful for detecting angiogenesis and detecting tumors or tumor invasion in a tissue ex vivo. The antagonist in this case is conjugated to fluorochrome, radioactive tag, paramagnetic heavy metal, diagnostic dye or enzyme. (1) is also useful for treating diabetic retinopathy, neovascular glaucoma, atherosclerotic plaques, osteoporosis, rheumatoid arthritis and other inflammatory diseases. The method are effective in part because the therapy is highly selective for angiogenesis and no other biological processes. Only new vessel growth is inhibited by antagonists that disrupt the localization of MMP-9, and therefore the therapeutic methods do not adversely affect mature vessels. Also, because certain of (1) affect only the localization of MMP-9, and do not directly block the proteolytic activity of MMP-9 or the adhesive functions of the beta1 integrins, it is likely that these compounds will have fewer side effects because the proteolytic activity of MMP-9 or the adhesive functions of the beta1 integrins may have normal physiological functions. The antagonists are highly potent suggesting that they may have therapeutic benefits at low concentrations

Sequence 10 AA;

Query Match 76.3%; Score 45; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLSGEPQC 10
1 CRLSGEPQC 10

RESULT 3
AAB70224
ID AAB70224 standard; protein; 2091 AA.

AC AAB70224;

DT 26-MAR-2002 (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 37464.

Drosophila developmental biology; cell signalling; insecticide; pharmacological.

Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEXE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PsDB; ABL14327.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 37464; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABR01840-ABR16175) and the encoded proteins (ABR57237-
 CC ABR72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2091 AA;

Query Match 71.2%; Score 42; DB 4; Length 2091;
 Best Local Similarity 88.9%; Pred. No. 4.9e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
 DB 1632 CRLRSGEPQ 1640

RESULT 4
 ADO41511
 ID ADO41511 standard; peptide; 236 AA.
 XX
 AC ADO41511;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Therapeutic bioconjugate-related integrin peptide #49.
 XX
 XX therapeutic bioconjugate; hydrophilic polymer; integrin;
 KW cell surface ligand; inflammatory bowel disease;
 KW sequelae of a bacterial infection; sepsis; septic shock;
 KW ischaemia-reperfusion injury; cancer metastasis; viper bite;
 KW rattlesnake bite.
 XX
 KM unidentified.
 OS
 XX
 PN WO2004045542-A2.
 XX
 PD 03-JUN-2004.
 XX
 PF 17-NOV-2003; 2003US-05036763.
 XX
 PR 15-NOV-2002; 2002US-00295734.
 XX
 PA (UYAR-) UNIV ARIZONA STATE.
 XX
 PI Massia SP, Ehteshami GR;
 XX
 DR WPI; 2004-440882/41.
 DR N-PsDB; ADO41510.
 XX
 PT Therapeutic bio-conjugate useful for treating thrombosis, or autoimmune

PT disease, has hydrophilic polymer, and one or more peptides capable of
 PT binding specifically to ligands expressed on a cell's surface.
 XX
 PS Claim 8; SEQ ID NO 98; 253pp; English.
 XX

XX The invention comprises a therapeutic bioconjugate that contains a
 CC hydrophilic polymer and one or more peptides (e.g. integrins) capable of
 CC binding specifically to a ligand expressed on a cell surface. The
 CC therapeutic bioconjugate of the invention is useful for preventing and
 CC treating inflammatory bowel disease, sequelae of a bacterial infection,
 CC sepsis, septic shock, ischaemia-reperfusion injury, cancer metastasis,
 CC and conditions caused by viper and rattlesnake bites. The present amino
 CC acid sequence represents an integrin peptide of the invention.
 XX

SQ Sequence 236 AA;
 Query Match 69.5%; Score 41; DB 8; Length 236;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPQ 9
 DB 2 RLRSGEPQ 9

RESULT 5
 ADP96089
 ID ADP96089 standard; protein; 236 AA.
 XX
 AC ADP96089;
 XX

DT 23-SEP-2004 (first entry)
 XX
 DE Human binding region from an integrin #50.
 XX

XX Human; integrin; binding region; bioconjugate; hydrophilic polymer;
 KW integrin alpha subunit; integrin beta subunit; thrombosis;
 KW atherosclerosis; systemic inflammatory response syndrome;
 KW multiple organ failure; autoimmune disease; inflammatory disease;
 KW allograft transplant rejection; Crohn's disease;
 KW inflammatory bowel disease; bacterial infection; sepsis; septic shock;
 KW ischaemia-reperfusion injury; cancer metastasis; viper bite;
 KW rattlesnake bite; cellular adhesion; migration; tumour metastasis;
 KW proliferation; angiogenesis; bone resorption; apoptosis.
 XX
 OS Homo sapiens.
 XX

XX Key Location/Qualifiers
 FH Modified-site 1
 FT Modified-site 1 /note="Optionally an N-terminal cysteine is added"
 FT Modified-site 236 /note="Optionally a C-terminal cysteine is added"
 FT
 XX
 PN US2004127416-A1.
 XX
 PD 01-JUL-2004.
 XX
 PF 17-NOV-2003; 2003US-00716293.
 XX
 PR 15-NOV-2002; 2002US-00295734.
 XX

PA (MASS/) MASSIA S P.
 XX
 PA (EHTE/) EHTESHAMI G R.
 XX

PI Massia SP, Ehteshami GR;
 XX
 DR WPI; 2004-524868/50.
 DR N-PsDB; ADP96088.
 XX

PT Bioconjugate useful for treating or preventing thrombosis,
 PT atherosclerosis, autoimmune disease, or inflammatory diseases comprises
 PT hydrophilic polymer, and peptides which bind specifically to ligand
 PT expressed on cell surface.

XX PS Claim 8; SEQ ID NO 99; 97bp; English.
 CC The invention relates to a bioconjugate (BC) comprising a hydrophilic
 CC polymer, and one or more peptides capable of binding specifically to a
 CC ligand expressed on the cell surface, in this case derived from integrin
 CC proteins. Also included are a nucleic acid (NA) having a sequence that
 CC encodes a peptide as mentioned in BC, a peptide (P) for preparing BC
 CC (having a sequence chosen from any one of 56 amino acids as given in the
 CC specification where each sequence comprises additionally an N-terminal
 CC and/or a C-terminal cysteine residue), a nucleic acid having the sequence
 CC that encodes (P), a kit (K) (comprising one or more of BC, reagent and
 CC apparatus suitable for administering BC to an individual), a biointerface
 CC formed on a mammalian tissue (comprising BC bound to several ligands on
 CC the tissue), preparing (M) a bioconjugate (involving (a) providing a
 CC hydrophilic polymer having one or more reactive groups, providing a
 CC bioselective peptide comprising a chemical group capable of reacting with
 CC the reactive groups, and contacting the polymer and the peptide under
 CC conditions, where the reactive and chemical groups react to form the
 CC bioconjugate or (b) providing a peptide chosen from any one of 109 amino
 CC acid sequences as given in the specification, modifying the peptide by
 CC addition of an N-terminal or C-terminal cysteine residue, providing an
 CC amount of activated dextran, and contacting the activated dextran and the
 CC modified peptide under conditions, where the dextran and the modified
 CC peptide react to form the bioconjugate), and therapeutic replacement
 CC fluids comprising BC and diluent. The peptide comprises the amino acid
 CC sequence of the binding portion of an integrin (alpha subunit or an
 CC integrin beta subunit). BC comprises one or more peptides chosen from any
 CC one of 101 amino acid sequences as given in the specification. The
 CC ligands comprise CN, I, CN, II, CN, III, CN, IV, the echovirus-1
 CC receptor, VCM-1, FN, MadCM-1, TSP, invasins, ICM-1, ICM-2, ICM-3, LPS,
 CC iCB, ICM-4, Fp, Factor X, CD23, NIF, heparin, heparin, LPS, Fp, VN,
 CC vWF, heparan, fibronectin, fibronectin, vitronectin, thrombospondin,
 CC von Willebrand factor, osteopontin, bone sialoprotein, laminins,
 CC collagens, neural cell adhesion molecule 1, or E-cadherin (cadherin-1).
 CC BC is useful for blocking interactions between cells in a living tissue,
 CC where the ligand is expressed on the surface of at least one of the
 CC cells, for blocking interactions between a cell and an extracellular
 CC matrix, where the ligand is capable of binding to a component of the
 CC matrix, for blocking pathological reactions triggered by cellular
 CC interactions in a living tissue, for blocking cell signaling
 CC receptors implicated in the regulation of cellular adhesion, migration,
 CC tumour metastasis, proliferation, angiogenesis, bone resorption,
 CC apoptosis, or gene expression, or for preventing adhesion of a mobile
 CC cell to a cell immobilised on a substrate. BC is useful for blocking
 CC pathological reactions triggered by cellular interactions in a living
 CC tissue. The above method is useful for preventing and treating
 CC thrombosis, atherosclerosis, systemic inflammatory response syndrome,
 CC multiple organ failure, autoimmune disease, inflammatory disease,
 CC allograft transplant rejection, Crohn's disease, inflammatory bowel
 CC disease, sequelae of a bacterial infection, sepsis or septic shock,
 CC ischaemia-reperfusion injury, cancer metastasis, or conditions caused by
 CC viper and rattlesnake bites. The present sequence is a Human ligand
 CC binding region from an integrin.
 XX SQ Sequence 236 AA;
 XX
 XX Query Match 69.5%; Score 41; DB 8; Length 236;
 XX Best Local Similarity 100.0%; Pred. No. 99;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 RLRSGEPO 9
 XX |||||
 XX Db 2 RLRSGEPO 9
 XX
 XX RESULT 6
 XX ABG70367
 XX ID ABG70367 standard; protein; 543 AA.
 XX AC ABG70367;
 XX DT 05-NOV-2002 (first entry)
 XX

XX DE Novel human thrombopoietin variant protein, NV-25.
 XX KW Human; splice variant; chromosome identification; cancer; thrombopoietin;
 XX KM thrombocytopenia; transporter protein.
 XX OS Homo sapiens.
 XX FN US2002068342-A1.
 XX PD 06-JUN-2002.
 XX PF 08-FEB-2001; 2001US-00778927.
 XX PR 09-FEB-2000; 2000IL-00134453.
 XX PR 29-MAR-2000; 2000IL-00135341.
 XX PA (KHOS/) KHOSRAVI R.
 XX (BERN/) BERNSTEIN J.
 XX PI Khosravi R, Bernstein J;
 XX PI WPI, 2002-592479/62.
 XX DR N-PsDB; ABS51840.
 XX XX Novel nucleic acid sequences that code for variants obtained by
 XX PT alternative splicing, homologs of known thrombopoietins, and homologs of
 XX PT transporter proteins, for treating diseases or disorders e.g.
 XX PT thrombocytopenia.
 XX PS Claim 6; Page 99-101; 114bp; English.
 XX
 XX The invention relates to novel nucleic acid (I) sequence of an
 XX alternative splicing variant and the amino acid sequence (II) encoded by
 XX (I). (I) is useful for a variety of diagnostic purposes and to detect and
 XX quantitate expression of the sequences in patient's cells e.g. biopsied
 XX tissues, for chromosome identification and for therapeutic purposes. The
 XX novel variants also serve for detection i.e. their presence or level
 XX indicates disease, disorder, pathological or normal condition or
 XX alternatively the ratio between the level of variants and the level of
 XX original sequence from which they were varied or the ratio to other
 XX variants may be indicative of a disease, disorder or pathological
 XX condition. The variants are useful for the development of pharmaceuticals
 XX for various pathological conditions in which cell cycle is not normal,
 XX notably cancer. Thrombopoietin (TH) product is useful for treating
 XX thrombocytopenia, transporter protein (TH) product is useful in
 XX conjunction with imaging substances for detection and imaging purposes.
 XX The variant product, the TH product or the TH product, its catalytic or
 XX immunogenic fragments or oligopeptides are useful for screening
 XX therapeutic compounds in a variety of drug screening techniques. ABG70342
 XX -ABG70381 represent novel human splice variant amino acid sequences of
 XX the invention
 XX SQ Sequence 543 AA;
 XX
 XX Query Match 69.5%; Score 41; DB 5; Length 543;
 XX Best Local Similarity 100.0%; Pred. No. 2,1e+02;
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 RLRSGEPO 9
 XX |||||
 XX Db 122 RLRSGEPO 129
 XX
 XX RESULT 7
 XX ABG70366
 XX ID ABG70366 standard; protein; 662 AA.
 XX AC ABG70366;
 XX DT 05-NOV-2002 (first entry)
 XX DE Novel human thrombopoietin variant protein, NV-25.
 XX


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XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US011647.
XX 01-MAY-1999; 99US-0132137P.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Geller HM, Melners S;
XX WPI; 2001-015974/02.
XX
XX New peptides and methods of stimulating axonal and/or dendritic growth
XX and/or guidance by administering a peptide, particularly comprising a
XX tenascin-C region, to a neuron.
XX
XX Disclosure; Page 20; 73pp; English.
XX
XX The present invention relates to a tenascin-C peptide. The peptide,
XX particularly from a tenascin-C region, is used for stimulating axonal
XX and/or dendritic growth, independent of neurite guidance, and stimulating
XX axonal and/or dendritic guidance independent of axonal and/or dendritic
XX growth
XX
XX Sequence 798 AA;
SQ
Query Match 69.5%; Score 41; DB 4; Length 798;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RLRSGEPQ 9
Db 122 RLRSGEPQ 129

```

RESULT 10
AAM39360
ID AAM39360 standard; protein: 798 AA.
AC AAM39360;
DT 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 2505.
FE
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-0048725.
XX 25-APR-2000; 2000US-0052317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-00653450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.

```

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AU, Yang Y, Zhang J, Zhao QA,
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX N-PSDB; AAI58516.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Example 4; SEQ ID NO 2505; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
SQ
Sequence 798 AA;
Qy 2 RLRSGEPQ 9
Db 122 RLRSGEPQ 129

```

RESULT 11
ABR81864
ID ABR81864 standard; protein: 798 AA.
AC ABR81864;
DT 18-SEP-2003 (first entry)
XX
XX Human integrin beta 1 subunit protein SEQ ID NO:2.
DE
XX Human; integrin alpha4beta1; fibronectin; integrin alpha 4; VCM;
XX integrin beta 1; vascular cell adhesion molecule; angiogenesis;
XX integrin alpha4beta1 binding inhibitor; angiogenesis inhibitor;
XX cytostatic; ophthalmological; antineoplastic; antiarthritic; cancer;
XX antiinflammatory; osteopathic; dermatological; gene therapy; psoriasis;
XX pathological condition; diabetic retinopathy; macular degeneration;
XX neovascularisation; rheumatoid arthritis; osteoarthritis; skin cancer;
XX endothelial progenitor cell; wound healing.
XX
XX Homo sapiens.
XX
XX WO2003019136-A2.
XX
XX 06-MAR-2003.
XX
XX 01-AUG-2002; 2002WO-US024573.
XX
XX 06-AUG-2001; 2001US-0310645P.
XX (REGC) UNIV CALIFORNIA.
XX Varner JA;
XX
XX WPI; 2003-278690/27.

DR N-PSDB; ACF03876.
 XX Inhibiting angiogenesis in a tissue, useful for treating cancer.
 PT arthritis, retinopathy, psoriasis; by providing a tissue and an agent
 PT that inhibits specific binding of integrin alpha-4beta-1 to an integrin
 PS alpha-4beta-1 ligand.
 XX Disclosure; Fig 7; 177p; English.
 PS
 CC The present invention describes a method for inhibiting angiogenesis in a
 CC tissue comprising providing a tissue and an agent that inhibits specific
 CC binding of integrin alpha4beta1 to an integrin alpha4beta1 ligand, and
 CC treating the tissue with the agent under conditions where the specific
 CC binding of the alpha4beta1 to the ligand is inhibited and a treated
 CC tissue is produced. Angiogenesis in the treated tissue is inhibited. Also
 CC described: (1) inhibiting endothelial cell adhesion or migration; (2)
 CC detecting angiogenesis in a tissue; (3) screening a test compound; (4)
 CC isolating endothelial progenitor cells from a tissue; and (5) reducing
 CC symptoms associated with cancer in a subject, or a pathological condition
 CC is an ocular or skin tissue. An integrin alpha4beta1 binding inhibitor
 CC has cyostatic, ophthalmological, antiinflammatory, antiarthritic,
 CC antiinflammatory, osteopathic and dermatological activities, and can be
 CC used in gene therapy. The methods are useful for treating cancer, and
 CC other pathological condition, such as diabetic retinopathy, macular
 CC degeneration by neovascularisation, rheumatoid arthritis, osteoarthritis,
 CC psoriasis or skin cancer. The methods are also useful in isolating
 CC endothelial progenitor cells, and in determining the mechanisms that
 CC underlie angiogenesis, development, wound healing and the function of the
 CC female reproductive system. The present sequence is used in the
 CC exemplification of the present invention
 CC
 SQ Sequence 798 AA;
 CC
 Query Match 69.5%; Score 41; DB 6; Length 798;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RLRSGEPO 9
 122 RLRSGEPO 129
 DB
 RESULT 12
 AB07462
 ID AB07462 standard; protein; 798 AA.
 XX
 AC AB07462;
 XX
 DT 28-JAN-2003 (first entry)
 XX
 DE Protein differentially regulated in prostate cancer #65.
 XX
 DE Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX
 OS Homo sapiens.
 XX
 PN WO200281638-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 08-APR-2002; 2002WO-US010824.
 XX
 PR 06-APR-2001; 2001US-0281731P.
 XX
 PR 06-APR-2001; 2001US-0281732P.
 XX
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX
 PI Sun Z, Jay G;
 XX
 PI
 XX
 DR MPI: 2003-058520/05.
 DR N-PSDB; ABX10364.
 DR

XX
 CC Novel genes which are differentially regulated in prostate cancer, useful
 CC PT for diagnosing prostate cancer in prostate tissue sample and assessing
 CC PT therapeutic or preventive intervention in prostate cancer patients.
 XX
 PS Claim 1; Page 334-337; 416pp; English.
 XX
 CC The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers as drug targets, and for detecting
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 CC
 SQ Sequence 798 AA;
 CC
 Query Match 69.5%; Score 41; DB 6; Length 798;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RLRSGEPO 9
 122 RLRSGEPO 129
 DB
 RESULT 13
 AB07412
 ID AB07412 standard; protein; 798 AA.
 XX
 AC AB07412;
 XX
 DT 28-JAN-2003 (first entry)
 XX
 DE Protein differentially regulated in prostate cancer #15.
 XX
 DE Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX
 OS Homo sapiens.
 XX
 PN WO200281638-A2.
 XX
 PD 17-OCT-2002.
 XX

PF 08-APR-2002; 2002MO-US010824.
 XX
 XX 06-APR-2001; 2001US-0281731P.
 PR 06-APR-2001; 2001US-0281732P.
 XX
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX
 PI Sun Z, Jay G;
 XX
 DR WPI; 2003-058520/05.
 XX
 PT Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.
 XX
 PS Claim 1; Page 240-242; 416pp; English.
 XX
 CC The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 XX
 SQ Sequence 798 AA;
 Query Match 69.5%; Score 41; DB 6; Length 798;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 8; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 2 RLRSGEPO 9
 DB 122 RLRSGEPO 129
 RESULT 14
 ADA21004
 ID ADA21004 standard; protein; 798 AA.
 AC ADA21004;
 XX 20-NOV-2003 (first entry)
 DT
 XX Human beta_1 polypeptide.
 DE
 XX

KW Integrin cell surface receptor; beta_6; cell adhesion;
 KW beta_6-containing integrin; human; beta_1.
 XX
 XX Homo sapiens.
 OS
 XX US2003064471-A1.
 PN
 XX 03-APR-2003.
 PD
 XX
 PF 14-AUG-2002; 2002US-00219631.
 XX
 PR 11-JUL-1991; 91US-00728215.
 PR 26-SEP-1997; 97US-0038085.
 PR 08-JUN-2000; 2000US-00591543.
 PR 06-FEB-2002; 2002US-00072841.
 XX
 PA (SHEP/) SHEPPARD D.
 PA (PYTEL/) PYTELA R.
 XX
 PI Sheppard D, Pytela R;
 XX
 DR WPI; 2003-540787/51.
 XX
 XX Novel substantially purified integrin cell surface receptor subunit
 PT comprising beta-6, useful for controlling cell adhesion in cells
 PT expressing a beta-6-containing integrin.
 XX
 PS Example 1; Fig 4; 46pp; English.
 XX
 CC The invention relates to a substantially purified integrin cell surface
 CC receptor subunit comprising a beta_6 polypeptide. The integrin cell
 CC surface receptor subunit is useful for increasing cell adhesion in cells
 CC expressing a beta-6-containing integrin, by overexpressing the beta-6-
 CC containing integrin in a cell. The subunit is useful for decreasing cell
 CC adhesion in cells expressing beta-6-containing integrin, by binding the
 CC integrin with a ligand. The subunit is also useful for detecting a ligand
 CC that binds the integrin, by contacting the integrin with a solution
 CC containing the ligand suspected of binding beta_6-containing integrins
 CC and detecting the presence of the ligand bound to the integrin. A reagent
 CC having specificity for beta 6 is useful as an immunogen, used to prepare
 CC reagents specific for beta 6 or as an indicator to detect beta_6-
 CC containing integrin. A nucleic acid encoding beta 6 is useful as a probe
 CC for diagnostic purposes. This sequence represents a human beta_1
 CC polypeptide.
 CC
 XX
 SQ Sequence 798 AA;
 Query Match 69.5%; Score 41; DB 7; Length 798;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RLRSGEPO 9
 DB 122 RLRSGEPO 129
 RESULT 15
 ADD46003
 ID ADD46003 standard; protein; 798 AA.
 AC ADD46003;
 XX 29-JAN-2004 (first entry)
 DT
 XX Human Protein Q14622, SEQ ID NO 11675.
 XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNL; Chung.
 XX
 XX Homo sapiens.
 OS
 XX WO2003016475-A2.
 PN

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